SEQUENCE LISTING

<110> CHERESH, David A.
      ELICEIRI, Brian
      SCHWARTZBERG, Pamela L.

<120> METHODS AND COMPOSITIONS USEFUL FOR MODULATION OF
      ANGIOGENESIS USING TYROSINE KINASE SRC

<130> TSRI 651.1

<140> US 09/701,500
<141> 2000-11-29

<150> PCT/US99/11780
<151> 1999-05-28

<150> US 60/087,220
<151> 1998-05-29

<160> 6

<170> PatentIn Ver. 2.0

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:RCASBP(A) based
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<223> pBR322 sequences

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<222> (1)..(101)
<223> upstream (numbering begins at the upstream R)

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<223> splice donor (AGGT)

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<222> (5074)..(5077)
<223> env splice acceptor (AGGC)

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<222> (6982)..(6985)
<223> ClaI splice acceptor (AGGA)
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<223> gag stop

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<223> env gp37


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<223> ClaI site/ the ClaI site in gag is methylated in
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gtgccttatt aggaaggcaa cagacgggtc tgacatggat tggacgaacc actgaattcc 11580

gcattgcaga gatattgtat ttaagtgcct agctcgatac aataaac        11627
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<210> 2
<211> 1759
<212> DNA
<213> Chicken


<220>

<221> gene
<222> (1)..(1759)
<223> chicken c-SRC cDNA


<220>

<221> CDS
<222> (112)..(1710)

<400> 2
 tctgacaccc atctgtctgt ctgtctgtgt gctgcaggag ctgagctgac tctgctgtgg 60

 cctcgcgtac cactgtggcc aggcggtagc tgggacgtgc agcccaccac c atg ggg   117
                                                             Met Gly
                                                              1


 agc agc aag agc aag ccc aag gac ccc agc cag cgc cgg cgc agc ctg    165
 Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg Ser Leu
             5               10                  15


 gag cca ccc gac agc acc cac cac ggg gga ttc cca gcc tcg cag acc    213
 Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser Gln Thr
         20              25                  30


 ccc aac aag aca gca gcc ccc gac acg cac cgc acc ccc agc cgc tcc    261
 Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser Arg Ser
  35              40                  45                  50


 ttt ggg acc gtg gcc acc gag ccc aag ctc ttc ggg ggc ttc aac act    309
 Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe Asn Thr
                 55                  60                  65


 tct gac acc gtt acg tcg ccg cag cgt gcc ggg gca ctg gct ggc ggc    357
 Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala Gly Gly
             70                  75                  80


 gtc acc act ttc gtg gct ctc tac gac tac gag tcc cgg act gaa acg    405
 Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr Glu Thr
             85                  90                  95


 gac ttg tcc ttc aag aaa gga gaa cgc ctg cag att gtc aac aac acg    453
 Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn Asn Thr
         100                 105                 110


 gaa ggt gac tgg tgg ctg gct cat tcc ctc act aca gga cag acg ggc    501
 Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln Thr Gly
 115                 120                 125                 130
```

```
tac atc ccc agt aac tat gtc gcg ccc tca gac tcc atc cag gct gaa    549
Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln Ala Glu
            135             140             145

gag tgg tac ttt ggg aag atc act cgt cgg gag tcc gag cgg ctg ctg    597
Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg Leu Leu
            150             155             160

ctc aac ccc gaa aac ccc cgg gga acc ttc ttg gtc cgg gag agc gag    645
Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu Ser Glu
            165             170             175

acg aca aaa ggt gcc tat tgc ctc tcc gtt tct gac ttt gac aac gcc    693
Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp Asn Ala
            180             185             190

aag ggg ctc aat gtg aag cac tac aag atc cgc aag ctg gac agc ggc    741
Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp Ser Gly
195             200             205             210

ggc ttc tac atc acc tca cgc aca cag ttc agc agc ctg cag cag ctg    789
Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln Gln Leu
            215             220             225

gtg gcc tac tac tcc aaa cat gct gat ggc ttg tgc cac cgc ctg acc    837
Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg Leu Thr
            230             235             240

aac gtc tgc ccc acg tcc aag ccc cag acc cag gga ctc gcc aag gac    885
Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp
            245             250             255

gcg tgg gaa atc ccc cgg gag tcg ctg cgg ctg gag gtg aag ctg ggg    933
Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly
            260             265             270

cag ggc tgc ttt gga gag gtc tgg atg ggg acc tgg aac ggc acc acc    981
Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr
275             280             285             290

aga gtg gcc ata aag act ctg aag ccc ggc acc atg tcc ccg gag gcc   1029
Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala
            295             300             305

ttc ctg cag gaa gcc caa gtg atg aag aag ctc cgg cat gag aag ctg   1077
Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu Lys Leu
            310             315             320

gtt cag ctg tac gca gtg gtg tcg gaa gag ccc atc tac atc gtc act   1125
Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr
            325             330             335

gag tac atg agc aag ggg agc ctc ctg gat ttc ctg aag gga gag atg   1173
Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly Glu Met
340             345             350

ggc aag tac ctg cgg ctg cca cag ctc gtc gat atg gct gct cag att   1221
Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile
355             360             365             370
```

```
gca tcc ggc atg gcc tat gtg gag agg atg aac tac gtg cac cga gac   1269
Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His Arg Asp
            375                 380                 385

ctg cgg gcg gcc aac atc ctg gtg ggg gag aac ctg gtg tgc aag gtg   1317
Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val
            390                 395                 400

gct gac ttt ggg ctg gca cgc ctc atc gag gac aac gag tac aca gca   1365
Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala
            405                 410                 415

cgg caa ggt gcc aag ttc ccc atc aag tgg aca gcc ccc gag gca gcc   1413
Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala
            420                 425                 430

ctc tat ggc cgg ttc acc atc aag tcg gat gtc tgg tcc ttc ggc atc   1461
Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile
435                 440                 445                 450

ctg ctg act gag ctg acc acc aag ggc cgg gtg cca tac cca ggg atg   1509
Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met
                455                 460                 465

gtc aac agg gag gtg ctg gac cag gtg gag agg ggc tac cgc atg ccc   1557
Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro
            470                 475                 480

tgc ccg ccc gag tgc ccc gag tcg ctg cat gac ctc atg tgc cag tgc   1605
Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys
            485                 490                 495

tgg cgg agg gac cct gag gag cgg ccc act ttt gag tac ctg cag gcc   1653
Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala
            500                 505                 510

ttc ctg gag gac tac ttc acc tcg aca gag ccc cag tac cag cct gga   1701
Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly
515                 520                 525                 530

gag aac cta taggcctgga gctcctcctg gaccagaggc ctcgctgtgg ggtacaggg  1759
Glu Asn Leu
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<210> 3
<211> 533
<212> PRT
<213> Chicken

<400> 3

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Met Gly Ser Ser Lys Ser Lys Pro Lys Asp Pro Ser Gln Arg Arg Arg
1               5                   10                  15

Ser Leu Glu Pro Pro Asp Ser Thr His His Gly Gly Phe Pro Ala Ser
            20                  25                  30
```

```
Gln Thr Pro Asn Lys Thr Ala Ala Pro Asp Thr His Arg Thr Pro Ser
        35              40                  45

Arg Ser Phe Gly Thr Val Ala Thr Glu Pro Lys Leu Phe Gly Gly Phe
    50              55                  60

Asn Thr Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly Ala Leu Ala
65              70                  75                      80

Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu Ser Arg Thr
            85                  90                      95

Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln Ile Val Asn
            100             105                 110

Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Thr Thr Gly Gln
        115                 120                 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp Ser Ile Gln
    130             135                 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu Ser Glu Arg
145             150                 155                     160

Leu Leu Leu Asn Pro Glu Asn Pro Arg Gly Thr Phe Leu Val Arg Glu
            165             170                 175

Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp
            180             185                 190

Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg Lys Leu Asp
        195             200                 205

Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Ser Ser Leu Gln
    210             215                 220

Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu Cys His Arg
225             230                 235                     240

Leu Thr Asn Val Cys Pro Thr Ser Lys Pro Gln Thr Gln Gly Leu Ala
            245                 250                 255

Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val Lys
            260             265                 270

Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly
    275             280                 285

Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro
    290             295                 300

Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu
305             310                 315                     320

Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile
            325             330                 335
```

```
Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly
            340             345             350

Glu Met Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala
            355             360             365

Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His
            370             375             380

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys
385                 390             395                 400

Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr
                405             410             415

Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu
            420             425             430

Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe
            435             440             445

Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro
    450             455             460

Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg
465             470             475                 480

Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys
            485             490             495

Gln Cys Trp Arg Arg Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu
            500             505             510

Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln
            515             520             525

Pro Gly Glu Asn Leu
    530
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<210> 4
<211> 2187
<212> DNA
<213> Homo sapiens

<220>
<221> gene
<222> (1)..(2187)
<223> human c-SRC cDNA

<220>
<221> CDS
<222> (134)..(1483)

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<400> 4
 gcgccgcgtc ccgcaggccg tgatgccgcc cgcgcggagg tggcccggac cgcagtgccc 60

 caagagagct ctaatggtac caagtgacag gttggcttta ctgtgactcg gggacgccag 120

 agctcctgag aag atg tca gca ata cag gcc gcc tgg cca tcc ggt aca      169
             Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
              1               5                  10

 gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg      217
 Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
            15              20                  25

 ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac      265
 Pro Phe Cys Lys Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp
        30                  35                  40

 ccc aac tgg tac aaa gcc aaa aac aag gtg ggc cgt gag ggc atc atc      313
 Pro Asn Trp Tyr Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile
 45                  50                  55                  60

 cca gcc aac tac gtc cag aag cgg gag ggc gtg aag gcg ggt acc aaa      361
 Pro Ala Asn Tyr Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys
                65                  70                  75

 ctc agc ctc atg cct tgg ttc cac ggc aag atc aca cgg gag cag gct      409
 Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala
            80                  85                  90

 gag cgg ctt ctg tac ccg ccg gag aca ggc ctg ttc ctg gtg cgg gag      457
 Glu Arg Leu Leu Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu
            95                  100                 105

 agc acc aac tac ccc gga gac tac acg ctg tgc gtg agc tgc gac ggc      505
 Ser Thr Asn Tyr Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly
     110                 115                 120

 aag gtg gag cac tac cgc atc atg tac cat gcc agc aag ctc agc atc      553
 Lys Val Glu His Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile
 125                 130                 135                 140

 gac gag gag gtg tac ttt gag aac ctc atg cag ctg gtg gag cac tac      601
 Asp Glu Glu Val Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr
                145                 150                 155

 acc tca gac gca gat gga ctc tgt acg cgc ctc att aaa cca aag gtc      649
 Thr Ser Asp Ala Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val
                160                 165                 170

 atg gag ggc aca gtg gcg gcc cag gat gag ttc tac cgc agc ggc tgg      697
 Met Glu Gly Thr Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp
            175                 180                 185

 gcc ctg aac atg aag gag ctg aag ctg ctg cag acc atc ggg aag ggg      745
 Ala Leu Asn Met Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly
     190                 195                 200
```

```
gag ttc gga gac gtg atg ctg ggc gat tac cga ggg aac aaa gtc gcc    793
Glu Phe Gly Asp Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala
205             210             215             220

gtc aag tgc att aag aac gac gcc act gcc cag gcc ttc ctg gct gaa    841
Val Lys Cys Ile Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu
            225             230             235

gcc tca gtc atg acg caa ctg cgg cat agc aac ctg gtg cag ctc ctg    889
Ala Ser Val Met Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu
        240             245             250

ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac    937
Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
        255             260             265

atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca    985
Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
    270             275             280

gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag   1033
Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
285             290             295             300

gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct   1081
Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
                305             310             315

gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac   1129
Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
            320             325             330

ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg   1177
Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu
        335             340             345

cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc   1225
Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
        350             355             360

act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac   1273
Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
365             370             375             380

tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc   1321
Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
            385             390             395

cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg   1369
Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
            400             405             410

ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc   1417
Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
        415             420             425
```

```
atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa   1465
Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
    430                 435                 440

acc cac gag ctg cac ctg tgacggctgg cctccgcctg ggtcatgggc          1513
Thr His Glu Leu His Leu
445                 450


ctgtggggac tgaacctgga agatcatgga cctggtgccc ctgctcactg ggcccgagcc 1573

tgaactgagc cccagcgggc tggcgggcct ttttcctgcg tcccagcctg caccctccg  1633

gccccgtctc tcttggaccc acctgtgggg cctggggagc ccactgaggg gccagggagg 1693

aaggaggcca cggagcggga ggcagcgccc caccacgtcg ggcttccctg cctcccgcc  1753

actcgccttc ttagagtttt attcctttcc tttttgaga  ttttttttcc gtgtgtttat 1813

tttttattat ttttcaagat aaggagaaag aaagtaccca gcaaatgggc attttacaag 1873

aagtacgaat cttatttttc ctgtcctgcc cgtgagggtg ggggggaccg ggcccctctc 1933

tagggacccc tcgccccagc ctcattcccc attctgtgtc ccatgtcccg tgtctcctcg 1993

gtcgccccgt gtttgcgctt gaccatgttg cactgtttgc atgcgcccga ggcagacgtc 2053

tgtcaggggc ttggatttcg tgtgccgctg ccacccgccc acccgccttg tgagatggaa 2113

ttgtaataaa ccacgccatg aggacaccgc cgcccgcctc ggcgcttcct ccaccgaaaa 2173

aaaaaaaaaa aaaa                                                   2187
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<210> 5
<211> 450
<212> PRT
<213> Homo sapiens

<400> 5

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Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
 1               5                  10                  15

Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
            20                  25                  30

Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
            35                  40                  45

Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
        50                  55                  60

Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65                  70                  75                  80
```

```
Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
            85          90              95

Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
            100             105             110

Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
            115             120             125

Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
    130             135             140

Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145             150             155             160

Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
            165             170             175

Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
            180             185             190

Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
            195             200             205

Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
    210             215             220

Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225             230             235             240

Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
            245             250             255

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
            260             265             270

Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
            275             280             285

Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
    290             295             300

Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305             310             315             320

Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
            325             330             335

Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
            340             345             350

Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
            355             360             365

Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
    370             375             380
```

```
Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385             390             395                     400

Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
                405             410                 415

Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
                420             425                 430

Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
            435             440             445

His Leu
    450


<210> 6
<211> 14
<212> PRT
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence:9E10-myc
      epitope tag

<400> 6
 Val Asp Met Glu Gln Lys Leu Ile Ala Glu Glu Asp Leu Asn
  1               5                   10
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